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Bio-diversity Studies on Accessions of African Yam Bean (*Sphenostylis stenocarpa*)

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ABSTRACT

African Yam Bean (AYB) is an underutilized crop with immense nutritional value derivable from both the seeds and tubers. This crop is relegated to an unimportant crop with bulk of the genetic resources left in the hands of older generations of farmers. Some AYB produce both seed and tuber. The aim of this research is to identify appropriate genotype grouping technique usable in classifying extent of diversity in accessions of AYB. Fifty accessions of African Yam Bean from diverse eco-geographic origins of Nigeria were grown in the Teaching and Research Farm of Ladoke Akintola University of Technology, Ogbomoso during the cropping seasons of May to November, 2009 and 2010. Randomised Complete Block Design (RCBD) with three replications were used. The first six principal components jointly explained 70.30% of the total variation among the accessions. Vine length, branching pattern, pod and peduncle number, pod length, seed number and seed yield contributed mostly to the tuber and seed yield variations. In all, Principal Component Analysis (PCA), Single Linkage Cluster Analysis (SLCA) and Unweighted Paired Group Method using Arithmetic average (UPGMA) identified eight major groups of the total variations. SLCA provided vivid information on accession grouping, using the crop morphology. The Genotype×Environment interaction revealed genotype to account for 54.2%, environment 10.5% and Genotype×Environment to account for 30.1% of the interaction sum of squares. Number of pods per plant, vine length and branch number contributed directly to seed yield. The genotypic co-efficient of variation (GCV) identified seed number per plant, pod length, number of filled pod and seed yield per plant to show significant variation with high heritability estimate. Selection focus on these traits will improve the seed yield in African Yam Bean.

Key words: Yam bean, seed yield, bio-diversity, morphological characterization

INTRODUCTION

African yam bean (*Sphenostylis stenocarpa*-Hochst Ex A. Rich), belongs to the family Fabaceae, sub-family Papilionoideae and a vigorous, herbaceous, climbing vine, reaching 2-3 m in height. It is one of the endangered African crop species that has immense nutritional advantages required in human diet. It has dual crop advantage as it produces both seed and tubers. Seed and tuber yield are inversely related (Ene-Obong and Okoye, 1992). At present, African Yam Bean has been relegated to an unimportant underutilized crop, predominantly grown by the older generation of farmers, leaving a bulk of the genetic resources of this crop in the hands of these farmers which threatens its survival (Saka *et al.*, 2004). Even though, the seed yielding type produce more yield than the tuber type, highest yields are obtained in mixed cropping with yam, maize, okra and other

vegetables. Crop improvement centers on identification of high yielding crop type (Aremu, 2011). Aremu *et al.* (2007) and Khodadad *et al.* (2011) respectively discovered genetic diversity measurement as a major tool exploitable in indentifying genetic variability and parent source for hybridization with the aim of improving crop yield performance. In breeding programs designed for improving African yam bean, hybridization and subsequent selection are important approaches. To achieve this, it is therefore important to identify genetic distance before parent selection (Joshi *et al.*, 2004). Higher genetic distance between parents confers higher heterosis in the resultant progenies (Aremu, 2011; Rameeh, 2011). If the genetic variability of any crop specie is carefully exploited, same is capable of providing critical bases for improving the grain yield as well as other economic and important traits (Inamullah *et al.*, 2006; Mahmood *et al.*, 2003). Moreover, an analysis of the association between various plant characters would help in identifying traits that are more important than the other (Azeez and Morakinyo, 2011).

This study attempts the assessment of the genetic relationships among 50 accessions AYB using morphological characterization.

MATERIALS AND METHODS

The research was carried out in the experimental field of Agronomy Department Ladoke Akintola University of Technology (LAUTECH), Ogbomoso during the 2009 and 2010 planting seasons. Using a Randomised Complete Block Design (RCBD) with four replications, fifty accessions of African Yam Bean (TSs-1, TSs-3, TSs-4, TSs-5, TSs-7, TSs-8, TSs-9, TSs-10, TSs-11, TSs-23, TSs-24, TSs-33, TSs-38, TSs-48, TSs-49, TSs-57, TSs-58, TSs-60, TSs-61, TSs-69, TSs-79, TSs-82, TSs-84, TSs-86, TSs-89, TSs-93, TSs-94, TSs-95, Tss-96, Tss-101, Tss-109, Tss-111, TSs-116, Tss-118, Tss-121, Tss-125, Tss-128, Tss-137, Tss-138, Tss-139, Tss-148, Tss-150, TSs-152, TSs-153, TSs-154, TSs-155, TSs-156, TSs-163, TSs-349 and TSs-373), sourced from the germplasm unit of the International Institute of Tropical Agriculture (IITA) Ibadan, were sown. Plot size was 5×5 m with inter and intra-row spacing of 1×1 m. Three seeds were sown per hole and later thinned to one plant stand fourth Weeks after Planting (WAP), to give a total of 25 plant stands per bed. The trailing stems were staked at eighth WAP. During the vegetative, seed and tuber growth phases, data were collected on 23 traits. At maturity, the dried matured pods were first harvested four weeks later the tubers were harvested.

Statistical analysis

Cluster analysis: This involves the use of multivariate techniques, with the primary purpose of grouping individuals based on morphometric characteristics, such that individuals with similar descriptions are mathematically brought together into the same cluster (Hair *et al.*, 1995). Clusters that resulted from individuals exhibited a high internal homogeneity and high external heterogeneity. The cluster analysis which includes Single Linkage (SLCA) and the Unweighted Paired Group Method using Arithmetic average (UPGMA), is used to decrease the number of individual characters, by sorting such into groups, with the aim of minimizing loss of information (Rhodes and Martins, 1972). The SLCA gives a hierarchical classification of homogenous multivariate characters and uses the coefficient of similarity to form a dendrogram (Sneath and Sokal, 1973). Through a successful classification, individuals within a cluster shall be closer when plotted geometrically and different clusters shall be further apart (Hair *et al.*, 1995).

Principal component (PC) analysis: PC analysis is a method of data reduction, to clarify the relationship between two or more characters and to divide the total variance of the original

characters into a limited number of uncorrelated new variables (Wiley, 1981). This allowed for visualization of the differences among the individuals and identify possible groups (Mohammadi and Prasanna, 2003; Aremu *et al.*, 2007). The reduction is thus achieved by linear transformation of the original variables into a new set of uncorrelated variables, known as principal components (PCs). PCs are orthogonal and independent of each other, each revealing different properties of the original data and may be interpreted independently, the total variation in the original data set may be broken down into components that are cumulative (Mohammadi and Prasanna, 2003).

The aim in the use of both cluster and PCs analyses is to identify any genetic distance between the accessions in use. According to Weir (1996) and Beaumont *et al.* (1998), such distance using morphological traits is calculated as thus:

$$d(i,j) = [(x_1-y_1)^2+(x_2-y_2)^2+.... (x_p-y_p)^2]^{1/2}$$

where, i and j is the distance between two individual accessions having morphological traits (p) x_1, x_2, \dots, x_p is the traits for i individuals and y_1, y_2, \dots, y_p is the traits for j individuals.

RESULT

Mean, ranges and analysis of variance: There were significant differences in the performance of the 50 accessions with reference to the significant mean square values for the twenty two traits studied (Table 1). Number of pods per plant, flower per plant, seed per pod, vine length, maturity period, number of seed per plant and seed yield per plant recorded highly significant mean square

Table 1: Mean, mean square (MS) and coefficient of variation of characters from 50 accessions of African yam bean

Character	Mean	Mean square	CV (%)
Number of peduncles	28.65	458.37*	74.52
Pods per peduncle	2.03	1.31*	264.59
Pod per plant	58.38	3377.60*	277.20
Filled pods per plant	15.41	470.79*	214.67
Number of flowers per plant	88.58	3862.99*	67.08
Length of pod	23.77	46.00*	88.30
Number of seeds per pod	20.04	7727.95	4360.63
100 seed weight (g)	19.36	56.13*	82.44
Days to sprouting	10.29	3.090*	69.38
Vine length at 8 weeks (cm)	108.44	1415.58*	71.10
Number of primary branches	2.68	0.65*	181.22
Number of secondary branches	6.65	3.95*	134.68
Days to flowering	112.71	48.13*	27.90
Days to maturity	162.42	10436.66	628.02
Internodal distance (cm)	12.37	47.65	537.05
Number of seeds per plant	222.59	128776.42*	330.39
Seed yield per plant (g)	41.51	3797.28*	387.22
Plant yield (kg ha ⁻¹)	518.83	593329.16*	387.19
Flower colour	2.00	0.00	0.00
Seed texture	3.90	0.37	0.00
Coat colour	5.35	0.93	0.00
Mottling	0.35	0.93	0.00

*Significant at p = 0.05

values. The quantitative characters showed wide to moderate variability. This is evident with seed and vegetative traits which recorded very high coefficients of variation. Number of pods per peduncle (264.59%), number of pods per plant (277.20%), number of filled pods per plant (214.67%), number of seeds per pod (4360.63%), days to maturity (628.02%), internode distance (537.05%), seed yield per plant (387.22%), plant yield (387.19%) and number of primary and secondary branches (181.22%; 134.68%), respectively.

PC analyses of the fifty African yam bean accessions studied: The first six principal components explained about 70.30% of the total variation (Table 2). Eigen values ranged from 5.99 in PC one (PC1) to 1.35 in principal component six. Seed yield traits were significant and accounted for more than a quarter (28.54%) of the total variation. PC2 which was largely controlled by branching pattern and seed quality accounted for 11.6%. Also, PC3, largely controlled by maturity date and morphological traits (such as the vine length and degree of mottling) accounted for 8.80% of the total variation, while PC4, 5 and 6 accounted for 7.96, 6.95 and 6.41%, respectively.

The first axis was loaded mainly by plant morphological quantitative traits of days to flowering and branching pattern (Table 3). The second principal component was loaded by seed yield and related traits; particularly pod length and weight of 100 seeds. The third principal component consisted basically of the tuber traits and the biochemical properties. The major characters of

Table 2: Eigen values, proportion of variation and contribution of 22 traits to total variation in the first six principal component axes of the 50 AYB accessions studied

Traits	PC1	PC2	PC3	PC4	PC5	PC6
Seed yield/plant	0.3679	-0.1302	0.0819	0.2205	-0.0267	-0.0233
Number of peduncles	0.2867	0.2514	-0.3278	-0.0152	0.1202	0.2008
Pods/peduncle	0.2100	-0.2521	0.1958	-0.2311	0.0389	-0.0723
Pod/plant	0.3647	0.0146	-0.1355	-0.1292	0.0973	0.0891
Filled pods	0.3850	-0.0415	0.0576	0.0032	0.1817	-0.0934
Flowers/plant	0.2897	0.2271	-0.3291	-0.0043	0.1064	0.2167
Pod length	-0.0263	-0.0664	0.1347	0.3840	0.3896	0.1609
Seed/pod	-0.0050	-0.1434	-0.1657	0.3507	-0.5466	0.0889
100 seed weight	-0.1509	-0.1963	0.0525	0.4438	0.1462	-0.0781
Days to sprouting	0.0140	-0.0083	0.0903	0.2302	0.0138	-0.4525
Vine length	0.1568	-0.0911	0.4297	0.0291	-0.0101	-0.0065
Primary branches	0.0028	0.5148	0.1643	0.0782	-0.0967	-0.1225
Sec. branches	0.0577	0.5328	0.0941	0.2346	-0.0355	-0.1930
Days to 50% flowering	-0.1848	0.0033	-0.1450	0.3364	0.1997	0.3899
Days to maturity	0.0220	0.2093	0.3499	0.2277	-0.0187	0.2942
Internode dist.	-0.0054	0.2021	-0.0307	0.0031	0.0462	-0.4356
Seeds/plant	0.3882	-0.0666	0.0536	0.1264	-0.0397	-0.0246
Plant yield (kg/ha)	0.3677	-0.1301	0.0819	0.2205	-0.0267	-0.0233
Seed texture	-0.0244	0.0234	0.1222	-0.1112	0.6372	-0.0844
Coat colour	-0.0172	0.2733	0.2880	-0.1302	-0.1257	0.2703
Mottling	0.0088	-0.0270	0.4345	-0.1994	-0.1114	0.2893
Eigen value	5.9900	2.4400	1.8500	1.6700	1.4600	1.3500
Percent variation	28.5400	11.6400	8.8000	7.9600	6.9500	6.4100
Cumulative	28.5400	40.1800	48.9800	56.9400	63.8900	70.3000

Table 3: Eigen vector of major traits of the first principal components axis used in ordination

Axis 1		Axis 2		Axis 3	
Character	Score	Character	Score	Character	Score
Vine length	0.19	No of peduncles	0.31	Tuber weight	0.27
Primary branches	0.27	Pods per peduncle	0.19	Crude protein	0.30
Secondary branches	0.27	Length of pod	0.35	Crude fiber	0.25
Internodal distance	0.23	Seeds per plant	0.23	Calcium	0.25
Days to flowering	-0.27	100 seed weight	-0.27	Moisture content	0.21

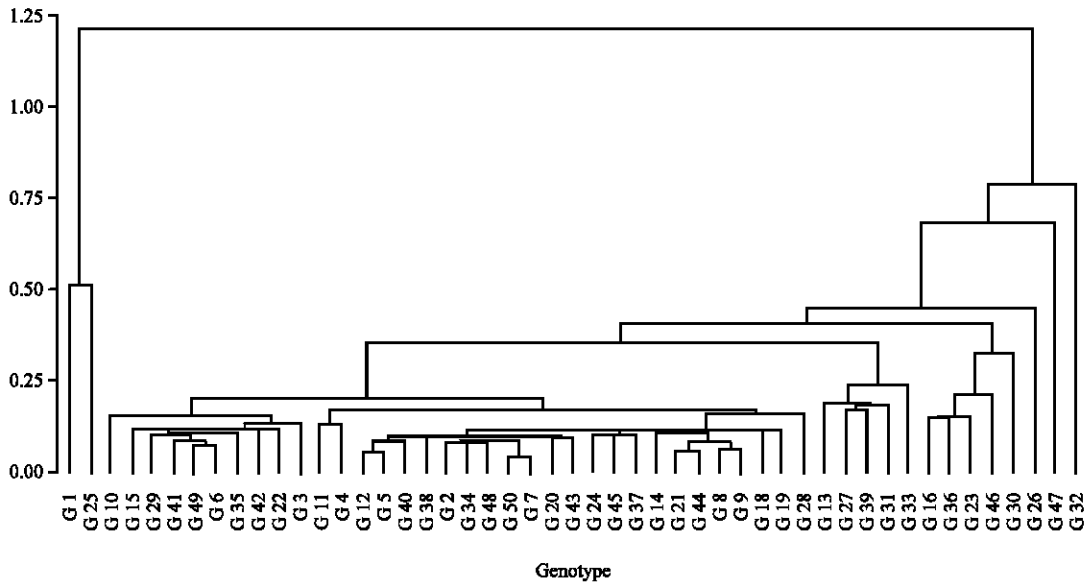


Fig. 1: Dendrogram from the SLCA of the 50 African yam bean accessions

interest in the three axes are the number of primary branches, number of secondary branches and days to flowering (0.27, 0.27, -0.27); 100 seed weight and number of peduncles (0.35, 0.31) and also crude protein and tuber weight (0.30, 0.27), respectively.

Dendrogram from SLCA and UPGMA average of the 50 African yam bean accessions: At 100% level of similarity (Fig. 1), there were two distinct clusters. Accessions G1 and G25 formed a single but distinct cluster, while accessions G10 to G32 jointly formed a separate cluster. Similarly, at 75% level of similarity, three separate and distinct clusters were formed; accessions G1 and G25 forming a single cluster still. Also, at this level, accessions G10 to G47 clustered together to form a single group, while accession G32 singly formed a distinct and separate cluster. However, at 50%, the 50 accessions clustered into five distinct groups. Here, accessions G10 to G26 jointly combined to form a single cluster, while accessions G1, G25, G47 and G32 individually formed separate and distinct clusters, respectively. Using UPGMA, at 100% level of similarity, three distinct and separate clusters were formed by the 50 African yam bean accessions (Fig. 2). Accessions G1 and G20 formed a distinct cluster, while accessions G10 to G48 jointly formed a separate cluster. Also, accessions G13 to G30 jointly formed another distinct cluster. Furthermore, at 50% level of similarity, six distinct clusters were formed. Accessions G1 and G25

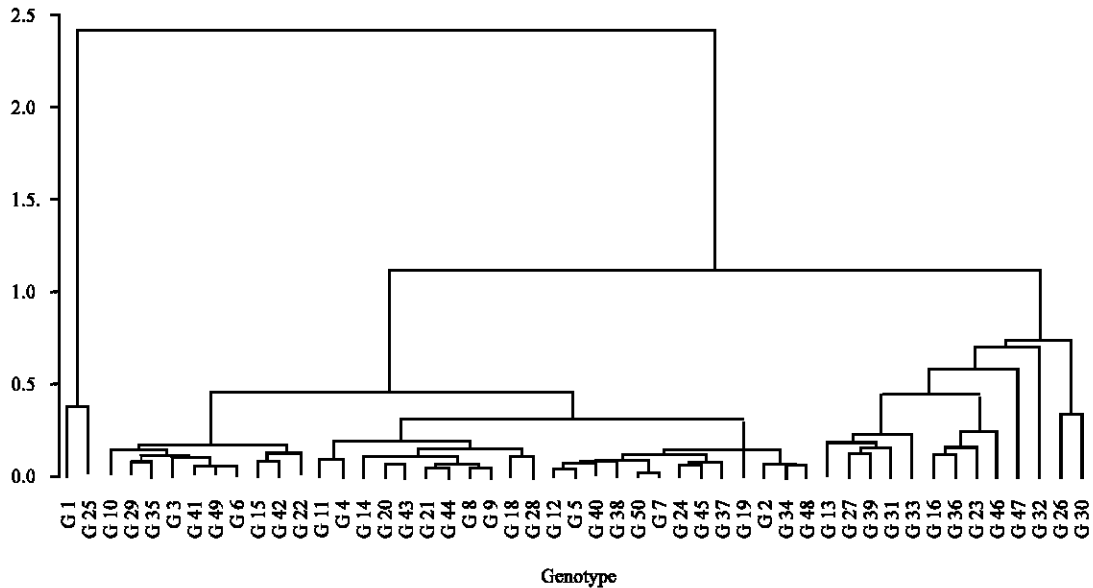


Fig. 2: Dendrogram from the UPGMA of the 50 African yam bean accessions

combined together to form a cluster. Also, accessions G10 to G48 clustered to form a separate group. Likewise, accessions G13 to G46 combined to form a separate cluster. Accessions G26 and G30 jointly formed a distinct cluster. However, accessions G47 and G32 individually formed distinct and separate clusters, respectively.

DISCUSSION

The role of physiological traits in grouping plant accessions is important and cannot be over-emphasized (Upadhyay *et al.*, 2011). The relatively high variations observed in pods per peduncle, pod per plant, number of filled pods, number of seeds per pod and days to pod maturity were indicative of varietal differences among the African yam bean accessions. Accessions with higher values of vine length, primary and secondary branches, number of peduncles and number of flowers produced higher number of pods and subsequently higher number of seeds per plant. The findings of Aremu *et al.* (2007) in their earlier work using cowpea supported this result. The relatively high number of flowers per peduncle produced by G13, G19, G23, G16 and G36, though aborted at early stages of development, are indicative of high floral productivity and hence, high seed yield, if flower abortion is controlled.

From the first six axes, above 70% of total variation in the accessions were explained even as the third axis identified tuber biochemical properties to contribute to the variations among the accessions. Principal component analysis and cluster analysis allowed grouping of the African yam bean accessions, consequently, the use of different measurement techniques can be appropriately used for grouping (Bauer *et al.*, 2007). Highest genetic distance was observed between G1 and G25 accessions. The report of Aremu *et al.* (2007), Brown-Guedira *et al.* (2000) and Rahim *et al.* (2010), agreed with this finding that accessions with maximum genetic distance resulted in high yield with hybrid vigor and that a cross between these accessions could be used in breeding programs to achieve maximum heterosis in cowpea, soybean and mungbean, respectively. Minimum distance was between accessions G50 and G7 which can be explored for backcross breeding programs.

Evaluation of genetic diversity can be useful for the selection of the most desirable and efficient accessions. Accordingly, if such effort results in the reduction of diversity, production of plants with higher uniformity may guarantee the production of enough food for the world's increasing population (Khodadad *et al.*, 2011). However, breeding strategies have not so far resulted very much in the increase in genetic diversity (Reif *et al.*, 2005; Fu, 2006).

CONCLUSION

The use of multivariate statistical technique is important in the classification of broad based accessions within germplasm collections. In African yam bean, the use of PCA resulted in the identification of both quantitative and qualitative characters that best described the variations between the accessions. Clustering revealed correlation between genetic diversity and eco-geographic background. It also revealed at a glance character performance based on accession groups. These variations within and between accessions would be of practical value, if the inter-character associations are known therefore, the various character performance are better determined under environmental and genetic influence.

The characters were variable and exhibited higher genotypic correlation relative to the phenotypic correlation, suggesting little or no environmental influence. The inter-character relationship would serve as a guide in formulating hybridization procedure to be employed for genotype selection. Genotype by environment interaction provided the opportunity to understand the performance of African yam bean genotypes over the planting environments. The genetic advance and realized heritability estimates are equally reliable and effective in selecting accessions for effective breeding programs.

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